

Seq ID NO:2 against mouse Doc4

RESULT 1

T14271

Doc4 protein, stress-induced - mouse

N;Alternate names: odz protein homolog

C;Species: Mus musculus (house mouse)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T14271

R;Wang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zinszner, H.; Ron, D. EMBO J. 17, 3619-3630, 1998

A;Title: Identification of novel stress-induced genes downstream of chop.

A;Reference number: Z17951; MUID:98315054; PMID:9649432

A;Accession: T14271

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-2825 <WAN>

A;Cross-references: EMBL:AF059485; NID:g3170614; PID:g3170615; PIDN:AAC31807.1

C;Genetics:

A;Gene: Doc4

Query Match 96.6%; Score 14306; DB 2; Length 2825;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 2655; Conservative 47; Mismatches 51; Indels 72; Gaps 2;

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Qy      1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
      |||
Db      1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKGPQKSYSSSETLKAYDQDARLAYGSRV 60

Qy     61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD 120
      ||:|||||
Db     61 KDMVPQEAEEFCRTGTNFTLRELGLGEMTPPHGTLYRTDIGLPHCGYSMGASSDADLEAD 120

Qy    121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTET----- 164
      |||
Db    121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDTEHENTETGAPLHCSSASSTPIEQ 180

Qy    165 -----DHPGGL 170
      |||
Db    181 SPSPPPSPPANESQRRLLGNGVAQPTPDSDEEEFVPNSFLVKSGSASLGAANDHPSSL 240

Qy    171 QNHARLRTPPPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPT D HSLSGEPPAGGAQ 230
      |||
Db    241 QNHPRLRTPPPLPHAHTPNQHHAASINSLNRGNFTPRSNPSPAPT D HSLSGEPPAGSAQ 300

Qy    231 EPAHAQENWLLNSNIPLERNLGKQPFLGTLQDNLIEMDILGASRHDGAYS D GHFLFKPG 290
      ||:|||||
Db    301 EPTHAQDNWVLNSKIPVETRNLGKQPFLGTWQDNLIEMDIFSASRRD GAYS D GHFFFKPG 360

Qy    291 GTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYCNWKAALSAIVIS 350
      |||
Db    361 GTSPLFCTTSPGYPLTSSTVYSPPPRPLPRSTFSRPAFNLKKPSKYCNWKAALSAILIS 420

Qy    351 ATLVILLAYFVAMHLFGLNWLQPMEG--QMYEITEDTASSWPVPTDVSLYPSGGTGLET 408
      |||
Db    421 ATLVILLAYFVAMHLFGLNWLQPMEGQM QMYEITEDTASSWPVPTDVSLYPSGGTGLET 480

Qy    409 PDRKGKGTEGKPSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNV 468
      |||
Db    481 PDRKGKGAAEGKPSLFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNV 540

Qy    469 SLGKAALVGIYGRKGLPPSHTQFDFVELLDGRRLLTQEARSLEGTPRQSRGTVPPSSHET 528
      |||
Db    541 SLGKAALVGIYGRKGLPPSHTQLDFVELLDGRRLLTQEARSLEGTPRQSRGTVPPSSHET 600

Qy    529 GFIQYLDSGIWHLAFYNDGKESEVVSFLT TAIESVDNCPSNCGNGDCISGTCHCFLGFL 588
      |||
Db    601 GFIQYLDSGIWHLAFYNDGKESEVVSFLT TAIESVDNCPSNCGNGDCISGTCHCFLGFL 660

Qy    589 GPDGGRASCPVLCSGNGQYMKGRCLCHSGWKAECDVPTNQCIDVACSNHGTCITGTCIC 648
      |||
Db    661 GPDGGRASCPVLCSGNGQYMKGRCLCHSGWKAECDVPTNQCIDVACSSHGTCIMGTCIC 720

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Qy	649	NPGYKGESCEEVD CMDPTCSGRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTF L P	708
Db	721	NPGYKGESCEEVD CMDPTCSSRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTF L P	780
Qy	709	DTGLCSDPSW TGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHPRCAEHG	768
Db	781	DTGLCNC DPSW TGHDCSIEICAADCGGHGVCVGGTCRCEDGWMGAACDQRACHPRCAEHG	840
Qy	769	TCRDGKCECSPGWNGEHCTIEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGAGCDTSMETA	828
Db	841	TCRDGKCECTPGWNGEHCTIEGCPGLCNGNGRCTLDLNGWHCVCQLGWRGTGCDTSMETG	900
Qy	829	CGDSKDNDGDGLVDCMDPDCC LQPLCHINPLCLGSPNPLDIIQETQVPVVSQQNLHSFYDR	888
Db	901	CGDGKDNDGDGLVDCMDPDCC LQPLCHVNPLCLGSPDPLDIIQETQAPVVSQQNLNSFYDR	960
Qy	889	IKFLVGRDSTHIIIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTISRQD	948
Db	961	IKFLVGRDSTHSIPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFINNPLFGYTISRQD	1020
Qy	949	GSFDLV TNGGISIIILRFERAPFITQEHTLWLPWDRFFVMETIIMRHEENEIPSCDLSNFA	1008
Db	1021	GSFDLV TNGGISIIILRFERAPFITQEHTLWLPWDRFFVMETIVMRHEENEIPSRDLSNFA	1080
Qy	1009	RPNPVVSPSPLTSFASSCAEKGPIVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRI	1068
Db	1081	RPNPVVSPSPLTSFASSCAEKGPIVPEIQALQEEIVIAGCKMRLSYLSSRTPGYKSVVRI	1140
Qy	1069	SLTHPTIPFNL MKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFLGSEAFVS	1128
Db	1141	SLTHPTIPFNL MKVHLMVAVEGRLFRKWFAAAPDLSYYFIWDKTDVYNQKVFLGSEAFVS	1200
Qy	1129	VG EY EY E S C P D L I L W E K R T T V L Q G Y E I D A S K L G G W S L D K H H A L N I Q S G I L H K G N G E N Q F V S	1188
Db	1201	VG EY EY E S C P D L I L W E K R T A V L Q G Y E I D A S K L G G W S L D K H H A L N I Q S G I L H K G N G E N Q F V S	1260
Qy	1189	Q Q P P V I G S I M G N G R R R S I S C P S C N G L A D G N K L L A P V A L T C G S D G S L Y V G D F N Y I R R I F P S	1248
Db	1261	Q Q P P V I G S I M G N G R R R S I S C P S C N G L A D G N K L L A P V A L T C G S D G S L Y V G D F N Y I R R I F P S	1320
Qy	1249	G N V T N I L E L S H S P A H K Y Y L A T D P M S G A V F L S D S N S R R V F K I K S T V V V K D L V K N S E V V A G T	1308
Db	1321	G N V T N I L E M S H S P A H K Y Y L A T D P M S G A V F L S D T N S R R V F K V K S T T V V K D L V K N S E V V A G T	1380
Qy	1309	G D Q C L F F D D T R C G D G G K A T E A T L T N P R G I T V D K F G L I Y F V D G T M I R R I D Q N G I I S T L L G S	1368
Db	1381	G D Q C L F F D D T R C G D G G K A T E A T L T N P R G I T V D K F G L I Y F V D G T M I R R V D Q N G I I S T L L G S	1440
Qy	1369	N D L T S A R P L S C D S V M D I S Q V H L E W P T D L A I N P M D N S L Y V L D N N V V L Q I S E N H Q V R I V A G R	1428
Db	1441	N D L T S A R P L S C D S V M E I S Q V R L E W P T D L A I N P M D N S L Y V L D N N V V L Q I S E N H Q V R I V A G R	1500
Qy	1429	P M H C Q V P G I D H F L L S K V A I H A T L E S A T A L A V S H N G V L Y I A E T D E K K I N R I R Q V T T S G E I S	1488
Db	1501	P M H C Q V P G I D Q F L L S K V A I H A T L E S A T A L A V S H N G V L Y I A E T D E K K I N R I R Q V T T S G E I S	1560
Qy	1489	L V A G A P S G C D C K N D A N C D C F S G D D G Y A K D A K L N T P S S L A V C A D G E L Y V A D L G N I R I R F I R	1548
Db	1561	L V A G A P S G C D C K N D A N C D C F S G D D G Y A K D A K L N T P S S L A V C A D G E L Y V A D L G N I R I R F I R	1620
Qy	1549	K N K P F L N T Q N M Y E L S S P I D Q E L Y L F D T T G K H L Y T Q S L P T G D Y L N F T Y T G D G D I T I T D N	1608
Db	1621	K N K P F L N T Q N M Y E L S S P I D Q E L Y L F D T S G K H L Y T Q S L P T G D Y L N F T Y T G D G D I T I T D N	1680
Qy	1609	N G N M V N V R R D S T G M P L W L V V P D G Q V Y W V T M G T N S A L K S V T T Q G H E L A M M T Y H G N S G L L A T	1668
Db	1681	N G N M V N V R R D S T G M P L W L V V P D G Q V Y W V T M G T N S A L R S V T T Q G H E L A M M T Y H G N S G L L A T	1740
Qy	1669	K S N E N G W T T F Y E Y D S F G R L T N V T F P T G Q V S S F R S D T D S S V H V Q V E T S S K D D V T I T T N L S A	1728
Db	1741	K S N E N G W T T F Y E Y D S F G R L T N V T F P T G Q V S S F R S D T D S S V H V Q V E T S S K D D V T I T T H L S G	1800

Qy	1729	SGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRNVTLP	1788
Db	1801	SGAFYTLQDQVRNSYYIGADGSLRLLLANGMEVALQTEPHLLAGTVNPTVGKRNVTLP	1860
Qy	1789	DNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKF	1848
Db	1861	DNGLNLVEWRQRKEQARGQVTVFGRRLRVHNRNLLSLDFDRVTRTEKIYDDHRKF	1920
Qy	1849	YDQAGRPSLWSPSSRLNGVNVTYSPGGYIAGIQRGIMSERMEYDQAGRITSRIFADGKTW	1908
Db	1921	YDQAGRPSFWSPSSRLNGVNVTYSPGGHIAGIQRGIMSERMEYDQAGRITSRIFADGKMW	1980
Qy	1909	SYTYLEKSMVLLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQPPEG	1968
Db	1981	SYTYLEKSMVLHLHLSQRQYIFEFDKNDRLSSVTMPNVARQTLETIRSVGYRNIYQPPEG	2040
Qy	1969	NASVIQDFTEDGHLLHTFYLGTRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTI	2028
Db	2041	NASVIQDFTEDGHLLHTFYLGTRRVIYKYGKLSKLAETLYDTTKVSFTYDETAGMLKTV	2100
Qy	2029	NLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNYDNSFRVTSMQAVINETPLP	2088
Db	2101	NLQNEGFTCTIRYRQIGPLIDRQIFRFTTEGMVNARFDYNYDNSFRVTSMQAVINETPLP	2160
Qy	2089	IDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHTKHFDAYGRMKEVQYEIFRSLMY	2148
Db	2161	IDLYRYDDVSGKTEQFGKFGVIYYDINQIITTAVMTHSKHFDAYGRMKEVQYETFRSLMY	2220
Qy	2149	WMTVQYDNMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLNGNLH	2208
Db	2221	WMTVQYDNMGRVVKELKVGYPYANTTRYSEYDADGQLQTVSINDKPLWRYSYDLNGNLH	2280
Qy	2209	LLSPGNSARLTPLRYDIRDRITRLGVDVQYKMEDEGFLRQGGDIFEYNSAGLLIKAYNRA	2268
Db	2281	LLSPGNSARLTPLRYDLRDRITRLGVDVQYKMEDEGSLRQGGDVFEYNSAGLLIKAYNRA	2340
Qy	2269	GSWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNPVKVTHLYNHSSEITSLYYDLQGH	2328
Db	2341	GSWSVRYRYDGLGRRVSSKSSSHHLQFFYADLTNPVKVTHLYSHSSEITSLYYDLQGH	2400
Qy	2329	LFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIIGYHG	2388
Db	2401	LFAMELSSGDEFYIACDNIGTPLAVFSGTGLMIKQILYTAYGEIYMDTNPNFQIIIGYHG	2460
Qy	2389	GLYDPLTKLVHMGRRDYDVLAGRWTSPDHLELWKHLSSSNVMPFNLYMFKNNNPISNSQDI	2448
Db	2461	GLYDPLTKLVHMGRRDYDVLAGRWTSPDHLELWKRLSSNSIVPFHLYMFKNNNPISNSQDI	2520
Qy	2449	KCFMTDVNSWLLTFGFLHNVIPGYPKPDMAMEPSYELIHTQMKTQEWDNSKSILGVQC	2508
Db	2521	KCFMTDVNSWLLTFGFLHNVIPGYPKPDTDAMEPSYELVHTQMKTQEWDNSKSILGVQC	2580
Qy	2509	EVQKQLKAFVTLERFDQLYGSTITSCQAPKTKKFASSGSVFGKGVKFAKDGRTTDII	2568
Db	2581	EVQKQLKAFVTLERFDQLYGSTITSCQAPETKFKFASSGSIFGKGVKFAKDGRTTDII	2640
Qy	2569	SVANEDGRRVAAILNHAHYLENLHFTIDGVDTHYFVKPGPSEGLAILGLSGGRRTLENG	2628
Db	2641	SVANEDGRRIAAILNNAHYLENLHFTIDGVDTHYFVKPGPSEGLAILGLSGGRRTLENG	2700
Qy	2629	VNVTVSQINTVLNGRTRRYTDIQLQYALCLNTRYGTTLDEEKARVLELARQAVRQAWA	2688
Db	2701	VNVTVSQINTMLSGRTRRYTDIQLQYALCLNTRYGTTVDEEKVRVLELARQAVRQAWA	2760
Qy	2689	REQQRLREGEGLRAWTEGEKQVVLSTGRVQGYDGFVVISVEQYPELSDSANNIHFMRQS	2748
Db	2761	REQQRLREGEGLRAWTDGEKQVVLNTGRVQGYDGFVTVSVEQYPELSDSANNIHFMRQS	2820
Qy	2749	EMGRR	2753

Db 2821 EMGRR 2825